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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,159A

DATE: 08/09/2002

TIME: 13:51:54

Input Set : A:\Lj5100.txt

Output Set: N:\CRF4\08092002\J032159A.raw

RECEIVED

AUG 28 2002

TECH CENTER 1600/2900

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4 <110> APPLICANT: Pawlowski, Krzysztof
5     Reed, John C.
6     Godzik, Adam
8 <120> TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
9     ENCODING NUCLEIC ACIDS, AND METHODS OF USE
12 <130> FILE REFERENCE: P-LJ 5100
14 <140> CURRENT APPLICATION NUMBER: US 10/032,159A
15 <141> CURRENT FILING DATE: 2001-12-19
17 <150> PRIOR APPLICATION NUMBER: US 60/257,457
18 <151> PRIOR FILING DATE: 2000-12-21
20 <160> NUMBER OF SEQ ID NOS: 37
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1101
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)...(1101)
33 <400> SEQUENCE: 1
34 atg tcg gac tac gag aac gat gac gag tgc tgg aac gtc ctg gag ggc      48
35 Met Ser Asp Tyr Glu Asn Asp Asp Glu Cys Trp Asn Val Leu Glu Gly
36 1          5          10          15
38 ttc cgg gtg acg ctc acc tcg gtc atc gac ccc tca cgc atc aca cct      96
39 Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro Ser Arg Ile Thr Pro
40          20          25          30
42 tac ctg cgg cag tgc aag gtc ctg aac cct gat gat gag gag cag gtg      144
43 Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp Asp Glu Glu Gln Val
44          35          40          45
46 ctc agc gac ccc aac ctg gtc atc cgc aaa cgg aaa gtg ggt gtg ctc      192
47 Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg Lys Val Gly Val Leu
48          50          55          60
50 ctg gac atc ctg cag cgg acc ggc cac aag ggc tac gtg gcc ttc ctc      240
51 Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly Tyr Val Ala Phe Leu
52 65          70          75          80
54 gag agc ctg gag ctc tac tac ccg cag ctg tac aag aag gtc aca ggc      288
55 Glu Ser Leu Glu Leu Tyr Tyr Pro Gln Leu Tyr Lys Lys Val Thr Gly
56          85          90          95
58 aag gag ccg gcc cgc gtc ttc tcc atg atc atc gac gcg tcc ggg gag      336
59 Lys Glu Pro Ala Arg Val Phe Ser Met Ile Ile Asp Ala Ser Gly Glu
60          100         105         110
62 tca ggc ctg act cag ctg ctg atg act gag gtc atg aag ctg cag aag      384
63 Ser Gly Leu Thr Gln Leu Leu Met Thr Glu Val Met Lys Leu Gln Lys

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64          115          120          125
66 aag gtg cag gac ctg acc gcg ctg ctg agc tcc aaa gat gac ttc atc 432
67 Lys Val Gln Asp Leu Thr Ala Leu Leu Ser Ser Lys Asp Asp Phe Ile
68          130          135          140
70 aag gag ctg cgg gtg aag gac agc ctg ctg cgc aag cac cag gag cgt 480
71 Lys Glu Leu Arg Val Lys Asp Ser Leu Leu Arg Lys His Gln Glu Arg
72 145          150          155          160
74 gtg cag agg ctc aag gag gag tgc gag gcc ggc agc cgc gag ctc aag 528
75 Val Gln Arg Leu Lys Glu Glu Cys Glu Ala Gly Ser Arg Glu Leu Lys
76          165          170          175
78 cgc tgc aag gag gag aac tac gac ctg gcc atg cgc ctg gcg cac cag 576
79 Arg Cys Lys Glu Glu Asn Tyr Asp Leu Ala Met Arg Leu Ala His Gln
80          180          185          190
82 agt gag gag aag ggc gcc gcg ctc atg cgg aac cgt gac ctg cag ctg 624
83 Ser Glu Glu Lys Gly Ala Ala Leu Met Arg Asn Arg Asp Leu Gln Leu
84          195          200          205
86 gag att gac cag ctc aag cac agc ctc atg aag gcc gag gac gac tgc 672
87 Glu Ile Asp Gln Leu Lys His Ser Leu Met Lys Ala Glu Asp Asp Cys
88          210          215          220
90 aag gtg gag cgc aag cac acg ctg aag ctc agg cac gcc atg gag cag 720
91 Lys Val Glu Arg Lys His Thr Leu Lys Leu Arg His Ala Met Glu Gln
92 225          230          235          240
94 cgg ccc agc cag gag ctg ctg tgg gag ctg cag cag gag aag gcc ctg 768
95 Arg Pro Ser Gln Glu Leu Leu Trp Glu Leu Gln Gln Glu Lys Ala Leu
96          245          250          255
98 ctc cag gcc cgg gtg cag gag ctg gag gcc tcc gtc cag gag ggg aag 816
99 Leu Gln Ala Arg Val Gln Glu Leu Glu Ala Ser Val Gln Glu Gly Lys
100          260          265          270
102 ctg gac agg agc agc ccc tac atc cag gta ctg gag gag gac tgg cgg 864
103 Leu Asp Arg Ser Ser Pro Tyr Ile Gln Val Leu Glu Glu Asp Trp Arg
104          275          280          285
106 cag gcg ctg cgg gac cac cag gag cag gcc aac acc atc ttc tcc ctg 912
107 Gln Ala Leu Arg Asp His Gln Glu Gln Ala Asn Thr Ile Phe Ser Leu
108          290          295          300
110 cgc aag gac ctc cgc cag ggc gag gcc cga cgc ctc cgg tgc atg gag 960
111 Arg Lys Asp Leu Arg Gln Gly Glu Ala Arg Arg Leu Arg Cys Met Glu
112 305          310          315          320
114 gag aag gag atg ttc gag ctg cag tgc ctg gca cta cgt aag gac tcc 1008
115 Glu Lys Glu Met Phe Glu Leu Gln Cys Leu Ala Leu Arg Lys Asp Ser
116          325          330          335
118 aag atg tac aag gac cgc atc gag gcc atc ctg ctg cag atg gag gag 1056
119 Lys Met Tyr Lys Asp Arg Ile Glu Ala Ile Leu Leu Gln Met Glu Glu
120          340          345          350
122 gtc gcc att gag cgg gac cag agc aca caa atg gag ggg ctg tga 1101
123 Val Ala Ile Glu Arg Asp Gln Ser Thr Gln Met Glu Gly Leu *
124          355          360          365
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 366
130 <212> TYPE: PRT

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```

131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 2
134 Met Ser Asp Tyr Glu Asn Asp Asp Glu Cys Trp Asn Val Leu Glu Gly
135 1 5 10 15
136 Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro Ser Arg Ile Thr Pro
137 20 25 30
138 Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp Asp Glu Glu Gln Val
139 35 40 45
140 Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg Lys Val Gly Val Leu
141 50 55 60
142 Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly Tyr Val Ala Phe Leu
143 65 70 75 80
144 Glu Ser Leu Glu Leu Tyr Tyr Pro Gln Leu Tyr Lys Lys Val Thr Gly
145 85 90 95
146 Lys Glu Pro Ala Arg Val Phe Ser Met Ile Ile Asp Ala Ser Gly Glu
147 100 105 110
148 Ser Gly Leu Thr Gln Leu Leu Met Thr Glu Val Met Lys Leu Gln Lys
149 115 120 125
150 Lys Val Gln Asp Leu Thr Ala Leu Leu Ser Ser Lys Asp Asp Phe Ile
151 130 135 140
152 Lys Glu Leu Arg Val Lys Asp Ser Leu Leu Arg Lys His Gln Glu Arg
153 145 150 155 160
154 Val Gln Arg Leu Lys Glu Glu Cys Glu Ala Gly Ser Arg Glu Leu Lys
155 165 170 175
156 Arg Cys Lys Glu Glu Asn Tyr Asp Leu Ala Met Arg Leu Ala His Gln
157 180 185 190
158 Ser Glu Glu Lys Gly Ala Ala Leu Met Arg Asn Arg Asp Leu Gln Leu
159 195 200 205
160 Glu Ile Asp Gln Leu Lys His Ser Leu Met Lys Ala Glu Asp Asp Cys
161 210 215 220
162 Lys Val Glu Arg Lys His Thr Leu Lys Leu Arg His Ala Met Glu Gln
163 225 230 235 240
164 Arg Pro Ser Gln Glu Leu Leu Trp Glu Leu Gln Gln Glu Lys Ala Leu
165 245 250 255
166 Leu Gln Ala Arg Val Gln Glu Leu Glu Ala Ser Val Gln Glu Gly Lys
167 260 265 270
168 Leu Asp Arg Ser Ser Pro Tyr Ile Gln Val Leu Glu Glu Asp Trp Arg
169 275 280 285
170 Gln Ala Leu Arg Asp His Gln Glu Gln Ala Asn Thr Ile Phe Ser Leu
171 290 295 300
172 Arg Lys Asp Leu Arg Gln Gly Glu Ala Arg Arg Leu Arg Cys Met Glu
173 305 310 315 320
174 Glu Lys Glu Met Phe Glu Leu Gln Cys Leu Ala Leu Arg Lys Asp Ser
175 325 330 335
176 Lys Met Tyr Lys Asp Arg Ile Glu Ala Ile Leu Leu Gln Met Glu Glu
177 340 345 350
178 Val Ala Ile Glu Arg Asp Gln Ser Thr Gln Met Glu Gly Leu
179 355 360 365
182 <210> SEQ ID NO: 3

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183 <211> LENGTH: 216
184 <212> TYPE: DNA
185 <213> ORGANISM: Homo sapiens
187 <220> FEATURE:
188 <221> NAME/KEY: CDS
189 <222> LOCATION: (1)...(216)
191 <400> SEQUENCE: 3
192 aac gtc ctg gag ggc ttc cgg gtg acg ctc acc tcg gtc atc gac ccc 48
193 Asn Val Leu Glu Gly Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro
194 1 5 10 15
196 tca cgc atc aca cct tac ctg cgg cag tgc aag gtc ctg aac cct gat 96
197 Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp
198 20 25 30
200 gat gag gag cag gtg ctc agc gac ccc aac ctg gtc atc cgc aaa cgg 144
201 Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg
202 35 40 45
204 aaa gtg ggt gtg ctc ctg gac atc ctg cag cgg acc ggc cac aag ggc 192
205 Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly
206 50 55 60
208 tac gtg gcc ttc ctc gag agc ctg 216
209 Tyr Val Ala Phe Leu Glu Ser Leu
210 65 70
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 72
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 4
219 Asn Val Leu Glu Gly Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro
220 1 5 10 15
221 Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp
222 20 25 30
223 Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg
224 35 40 45
225 Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly
226 50 55 60
227 Tyr Val Ala Phe Leu Glu Ser Leu
228 65 70
231 <210> SEQ ID NO: 5
232 <211> LENGTH: 432
233 <212> TYPE: DNA
234 <213> ORGANISM: Homo sapiens
236 <220> FEATURE:
237 <221> NAME/KEY: CDS
238 <222> LOCATION: (1)...(432)
240 <400> SEQUENCE: 5
241 ctg cgc aag cac cag gag cgt gtg cag agg ctc aag gag gag tgc gag 48
242 Leu Arg Lys His Gln Glu Arg Val Gln Arg Leu Lys Glu Glu Cys Glu
243 1 5 10 15
245 gcc ggc agc cgc gag ctc aag cgc tgc aag gag gag aac tac gac ctg 96

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```

246 Ala Gly Ser Arg Glu Leu Lys Arg Cys Lys Glu Glu Asn Tyr Asp Leu
247          20          25          30
249 gcc atg cgc ctg gcg cac cag agt gag gag aag ggc gcc gcg ctc atg 144
250 Ala Met Arg Leu Ala His Gln Ser Glu Glu Lys Gly Ala Ala Leu Met
251          35          40          45
253 cgg aac cgt gac ctg cag ctg gag att gac cag ctc aag cac agc ctc 192
254 Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu
255          50          55          60
257 atg aag gcc gag gac gac tgc aag gtg gag cgc aag cac acg ctg aag 240
258 Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys
259 65          70          75          80
261 ctc agg cac gcc atg gag cag cgg ccc agc cag gag ctg ctg tgg gag 288
262 Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu
263          85          90          95
265 ctg cag cag gag aag gcc ctg ctc cag gcc cgg gtg cag gag ctg gag 336
266 Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu
267          100          105          110
269 gcc tcc gtc cag gag ggg aag ctg gac agg agc agc ccc tac atc cag 384
270 Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln
271          115          120          125
273 gta ctg gag gag gac tgg cgg cag gcg ctg cgg gac cac cag gag cag 432
274 Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln
275          130          135          140
279 <210> SEQ ID NO: 6
280 <211> LENGTH: 144
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <400> SEQUENCE: 6
285 Leu Arg Lys His Gln Glu Arg Val Gln Arg Leu Lys Glu Glu Cys Glu
286 1          5          10          15
287 Ala Gly Ser Arg Glu Leu Lys Arg Cys Lys Glu Glu Asn Tyr Asp Leu
288          20          25          30
289 Ala Met Arg Leu Ala His Gln Ser Glu Glu Lys Gly Ala Ala Leu Met
290          35          40          45
291 Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu
292          50          55          60
293 Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys
294 65          70          75          80
295 Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu
296          85          90          95
297 Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu
298          100          105          110
299 Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln
300          115          120          125
301 Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln
302          130          135          140
305 <210> SEQ ID NO: 7
306 <211> LENGTH: 3744
307 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/09/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 416,417
Seq#:15; Xaa Pos. 139
Seq#:16; Xaa Pos. 139
Seq#:30; N Pos. 470
Seq#:33; N Pos. 42,85,109,111,139,222,244,263
Seq#:36; N Pos. 213

VERIFICATION SUMMARY

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L:1068 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:384
L:1102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:417
L:1133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:128
L:1522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:420
L:1569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:60
L:1571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:120
L:1572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:180
L:1573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:240
L:1611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:180